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BF

us-10-698-041-1.rnpb

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 10:58:17 ; Search time 877 Seconds
(without alignments)
9719.189 Million cell updates/sec

Title: US-10-698-041-1.
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1405	100.0	1405	18	US-10-698-041-1	Sequence 1, Appli

us-10-698-041-1.rnpb						
2	1003	71.4	1514	17	US-10-251-215-38	Sequence 38, Appl
3	985.8	70.2	1424	18	US-10-698-041-2	Sequence 2, Appli
4	958.4	68.2	5925	16	US-10-235-175-78	Sequence 78, Appl
5	923	65.7	1539	18	US-10-492-729-4	Sequence 4, Appli
6	916.6	65.2	1539	18	US-10-492-729-12	Sequence 12, Appl
7	884.8	63.0	10251	17	US-10-045-674-582	Sequence 582, App
8	856	60.9	1526	18	US-10-679-620-87	Sequence 87, Appl
9	851.8	60.6	1551	18	US-10-679-620-69	Sequence 69, Appl
10	834.8	59.4	1566	18	US-10-679-620-67	Sequence 67, Appl
11	834	59.4	2154	18	US-10-679-620-63	Sequence 63, Appl
12	820.8	58.4	1572	18	US-10-679-620-65	Sequence 65, Appl
13	820	58.4	2160	18	US-10-679-620-61	Sequence 61, Appl
14	779.8	55.5	6563	10	US-09-726-258-61	Sequence 61, Appl
15	739.6	52.6	1951	13	US-10-011-125-1	Sequence 1, Appli
16	739.6	52.6	6072	9	US-09-056-160B-99	Sequence 99, Appl
17	739.6	52.6	6072	16	US-10-234-671-99	Sequence 99, Appl
18	738.6	52.6	2143	9	US-09-940-166A-5	Sequence 5, Appli
19	738.6	52.6	2143	18	US-10-762-967-5	Sequence 5, Appli
20	734.6	52.3	6127	9	US-09-920-171-1	Sequence 1, Appli
21	734.6	52.3	6127	15	US-10-113-996-1	Sequence 1, Appli
22	734.6	52.3	6127	18	US-10-791-619-1	Sequence 1, Appli
23	732.8	52.2	1477	19	US-10-728-420B-116	Sequence 116, App
c 24	732.8	52.2	1477	19	US-10-728-420B-117	Sequence 117, App
25	681.6	48.5	1730	14	US-10-194-975-108	Sequence 108, App
26	628	44.7	720	17	US-10-292-088-15	Sequence 15, Appl
27	627.8	44.7	720	17	US-10-292-088-63	Sequence 63, Appl
28	624.8	44.5	720	17	US-10-292-088-7	Sequence 7, Appli
29	624.8	44.5	720	17	US-10-292-088-101	Sequence 101, App
30	624.4	44.4	720	17	US-10-292-088-55	Sequence 55, Appl
31	623.2	44.4	720	17	US-10-292-088-79	Sequence 79, Appl
32	621.6	44.2	720	17	US-10-292-088-39	Sequence 39, Appl
33	620	44.1	720	17	US-10-292-088-31	Sequence 31, Appl
34	618.8	44.0	4793	18	US-10-737-290-141	Sequence 141, App
35	612.6	43.6	1081	17	US-10-466-164-33	Sequence 33, Appl
36	612.2	43.6	657	10	US-09-972-656-103	Sequence 103, App
37	609.8	43.4	649	19	US-10-714-079C-8	Sequence 8, Appli
38	606.2	43.1	944	17	US-10-108-260A-1585	Sequence 1585, Ap
39	604.6	43.0	968	10	US-09-992-600A-7	Sequence 7, Appli
40	604.6	43.0	968	10	US-09-924-340-7	Sequence 7, Appli
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42	604.6	43.0	968	10	US-09-999-570-7	Sequence 7, Appli
43	604.6	43.0	968	14	US-10-000-489-7	Sequence 7, Appli
44	604.6	43.0	968	14	US-10-000-986-7	Sequence 7, Appli
45	604.6	43.0	968	16	US-10-154-678-7	Sequence 7, Appli

RESULT 2

US-10-251-215-38

; Sequence 38, Application US/10251215

; Publication No. US20030219839A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Kretz-Rommel, Anke

; APPLICANT: Frederickson, Shana

; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 1087-36

; CURRENT APPLICATION NUMBER: US/10/251,215

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: US 60/323,537

; PRIOR FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: US 60/323,544

; PRIOR FILING DATE: 2001-09-20

us-10-698-041-1.rnpb
 ; PRIOR APPLICATION NUMBER: US 60/379,980
 ; PRIOR FILING DATE: 2002-05-13
 ; NUMBER OF SEQ ID NOS: 79
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 38
 ; LENGTH: 1514
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Assembled Degenerate Oligonucleotides
 US-10-251-215-38

Query Match 71.4%; Score 1003; DB 17; Length 1514;
 Best Local Similarity 83.7%; Pred. No. 7e-281;
 Matches 1163; Conservative 25; Mismatches 165; Indels 36; Gaps 4;

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QY      35 GCGGCCGAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCG 94
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QY      95 GCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACTAATTTG 154
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DB      75 GTCACCATCACTTGCCRGGCSAGTCAGRGCATTAGT-----ARYTACTTA 119

QY     155 GATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTTTAAT 214
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     120 GCCTGGTATCAGCAGAAACCAGGGAAASYTCCTAAGCTCCTGATCTATGATGCATCCGAT 179

QY     215 CGGGCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTATACACTG 274
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DB     180 CTGGCATCTGGGGTCCCATCTCGGTTTCARTGGCAGTGGATCTGGGACAGATTWCACTCTC 239

QY     275 AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAG----- 326
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB     240 ACCATCAGCAGCCTGCAGYSTGAAGATGYTGCAACTTATTACTGTCAACAGGGTTATAGT 299

QY     327 -GTCTACAACTCCTAGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTG 385
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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QY     386 GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTCC 445
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DB     360 GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTCC 419

QY     446 TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG 505
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DB     420 TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG 479

QY     506 GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC 565
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DB     480 GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC 539

QY     566 AGCACCTACAGCCTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAA 625
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QY     626 GTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAAC 685
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QY     686 AGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGAATTTAAAATGAAATACCTATTG 745
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DB     660 AGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGAATTTAAAATGAAATACCTATTG 719

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Qy	806	CTGCAGGAGTCCGGGGGAGGCTTAGTTACGCTGGGGGGTCCCTGAGACTCTCCTGTGAA	865
Db	780	CTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCA	839
Qy	866	GCCTCTGGATACACCTTCAGCAATTACTGGATGCACTGGGTCCGCCAACCTCCAGGGAAG	925
Db	840	GCCTCTGGATTWCYCYCAGTARMWATRKMATRARYTGGGTCCGCCAGGCTCCAGGGAAG	899
Qy	926	GGGCTGGTGTGGGTCTCACGTATTAATGAAGATGGGAGTATCACAAACGACGCGGACTCC	985
Db	900	GGGCTGGAGTGGRTCKSATTCATTAAT---ACTGGTAGTAGCGCATACTACGCGAGCTGG	956
Qy	986	GTGAAGGGCCGATCCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGGAAATG	1045
Db	957	GCGGAAAGCCGATYCACCATCTCCAGAGACAMCGCCAAGAACTCASTGTATCTGCAAATG	1016
Qy	1046	AACAGTCTGAGAGCCGAGGACACGGCTGTCTATTACTGTACACGAGATATTGGGGGTCTG	1105
Db	1017	AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTWCTGTGCGAGAGGTAGTCCTGGTTAC	1076
Qy	1106	GATGCT-----CACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACC	1156
Db	1077	AGTGATGGACTTAACATCTGGGGCCAGGGCACCCCTGGTCACCGTCTCCTCAGCCTCCACC	1136
Qy	1157	AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG	1216
Db	1137	AAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCG	1196
Qy	1217	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA	1276
Db	1197	GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCA	1256
Qy	1277	GGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTAC	1336
Db	1257	GGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTAC	1316
Qy	1337	TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC	1396
Db	1317	TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC	1376
Qy	1397	AACGTGAAT	1405
Db	1377	AACGTGAAT	1385